

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: LONZA AG
- (B) STREET: Muenchensteinerstrasse 38
- (C) CITY: Basle
- (E) COUNTRY: Switzerland
- (F) POSTAL CODE: 4002

(ii) TITLE OF INVENTION: Process for the preparation of (S)- or (R)-3,3,3-trifluoro-2-hydroxy-2-methylpropionic acid

(iii) NUMBER OF SEQUENCES: 14 ✓

(iv) COMPUTER-READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1442 base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: Klebsiella oxytoca
- (B) STRAIN: PRS1
- (C) INDIVIDUAL/ISOLATE: PRS1

(vii) PROVENANCE:

- (B) CLONE(S): pPRS2a

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(197..1181)
- (D) OTHER INFORMATION:/product= "amidase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CCCCGGAACT CCATGTGGCC GTGATCCTGG TCGAGCAGGA TATTGGATG ATCCAGCGGG	60
CCGCACAGCG CTGTGCGGTA ATGGATAAAG GCCTGGTTGT AGAAACGCTG ACCCAACAAC	120
AGCTCTCTGA TGATCTTTTA ATGCGTCGTC ATCTGGCTCT GTAACAAAC GCTATAAATT	180
ACGTGGAGAA TAACAT ATG AAA TGG TTG GAA GAA TCC ATT ATG GCC AAA	229
Met Lys Trp Leu Glu Glu Ser Ile Met Ala Lys	
1	5
	10

CGC GGT GTT GGT GCC GGG CGT AAA CCG GTA ACG CAT CAC CTG ACG GAA Arg Gly Val Gly Ala Gly Arg Lys Pro Val Thr His His Leu Thr Glu 15 20 25	277
GAA ATG CAA AAA GAG TTT CAT TAC ACC ATT GGC CCT TAT TCC ACA CCC Glu Met Gln Lys Glu Ph His Tyr Thr Ile Gly Pro Tyr Ser Thr Pro 30 35 40	325
GTC CTG ACC ATC GAA CCC GGT GAC CGG ATT ATT GTC GAC ACT CGA GAT Val Leu Thr Ile Glu Pro Gly Asp Arg Ile Ile Val Asp Thr Arg Asp 45 50 55	373
GCT TTT GAA GGT GCT ATC AAT TCG GAA CAG GAT ATT CCG AGC CAG TTG Ala Phe Glu Gly Ala Ile Asn Ser Glu Gln Asp Ile Pro Ser Gln Leu 60 65 70 75	421
CTA AAA ATG CCC TTT CTC AAC CCA CAA AAC GGA CCG ATC ATG GTC AAT Leu Lys Met Pro Phe Leu Asn Pro Gln Asn Gly Pro Ile Met Val Asn 80 85 90	469
GGC GCG GAG AAA GGT GAT GTG CTC GCT GTC TAT ATC GAA TCC ATG TTG Gly Ala Glu Lys Gly Asp Val Leu Ala Val Tyr Ile Glu Ser Met Leu 95 100 105	517
CCC CGC GGC GTT GAT CCC TAC GGC ATC TGC GCC ATG ATT CCG CAT TTT Pro Arg Gly Val Asp Pro Tyr Gly Ile Cys Ala Met Ile Pro His Phe 110 115 120	565
GGC GGA CTG ACC GGG ACC GAC CTG ACG GCC ATG CTC AAT GAT CCG CTC Gly Gly Leu Thr Gly Thr Asp Leu Thr Ala Met Leu Asn Asp Pro Leu 125 130 135	613
CCA GAA AAG GTG CGC ATG ATT AAA CTC GAC AGT GAA AAG GTC TAC TG Pro Glu Lys Val Arg Met Ile Lys Leu Asp Ser Glu Lys Val Tyr Trp 140 145 150 155	661
AGC AAA CGC CAT ACG CTT CCC TAT AAA CCC CAT ATT GGC ACC TTG ACC Ser Lys Arg His Thr Leu Pro Tyr Lys Pro His Ile Gly Thr Leu Ser 160 165 170	709
GTA TCG CCA GAA ATT GAC TCA ATC AAT TCA CTG ACG CCA GAC AAT CAC Val Ser Pro Glu Ile Asp Ser Ile Asn Ser Leu Thr Pro Asp Asn His 175 180 185	757
GGC GGG AAT ATG GAT GTG CCG GAT ATA GGA CCA GGG AGT ATT ACC TAT Gly Gly Asn Met Asp Val Pro Asp Ile Gly Pro Gly Ser Ile Thr Tyr 190 195 200	805
CTG CCG GTA CGT GCG CCT GGA GGC CGC CTG TTT ATT GGT GAT GCC CAT Leu Pro Val Arg Ala Pro Gly Gly Arg Leu Phe Ile Gly Asp Ala His 205 210 215	853
GCT TGT CAG GGT GAT GGT GAG ATT TGC GGG ACC GCA GTA GAG TTT GCC Ala Cys Gln Gly Asp Gly Glu Ile Cys Gly Thr Ala Val Glu Phe Ala 220 225 230 235	901
TCA ATC ACC ACC ATC AAA GTC GAT TTG ATC AAG AAC TGG CAG CTT TCC Ser Ile Thr Thr Ile Lys Val Asp Leu Ile Lys Asn Trp Gln Leu Ser 240 245 250	949
TGG CCA CGA ATG GAG AAT GCC GAA AAT ATT ATG AGT ATT GGC AGT GCA Trp Pro Arg Met Glu Asn Ala Glu Asn Ile Met Ser Ile Gly Ser Ala 255 260 265	997

CGT CCG CTG GAG GAT GCG ACG CGA ATT GCA TAT CGC GAC TTA ATT TAC Arg Pro Leu Glu Asp Ala Thr Arg Ile Ala Tyr Arg Asp Leu Ile Tyr 270 275 280	1045
TGG CTG GTA GAA GAC TTT GGC TTC GAA CAA TGG GAT GCC TAC ATG CTT Trp Leu Val Glu Asp Phe Gly Phe Glu Gln Trp Asp Ala Tyr Met Leu 285 290 295	1093
CTG AGT CAA TGC GGC AAA GTG CGG CTG GGC AAC ATG GTC GAC CCC AAA Leu Ser Gln Cys Gly Lys Val Arg Leu Gly Asn Met Val Asp Pro Lys 300 305 310 315	1141
TAC ACC GTT GGC GCG ATG CTG AAC AAA AAC CTG TTA GTT TAGTAGGAAT Tyr Thr Val Gly Ala Met Leu Asn Lys Asn Leu Leu Val 320 325	1190
AACTAACCCGG TGAACATTAC CCCGGATGTAG ATCGGGTAA TGTGTAAGTT CAAACAATCG CTATTTTAA CAGCTAAAGC AGGTGCATAT GGGGCCAGAT ACACCCATCA ATATTGGTTT ACTTTACTCC TTCAGCGGAG TGACGGCGGC ACAAGAGTTG TCACAATGGC GCGGAGCAAC CCAGGCTATT GCCGAAATTA ATCAAAATGG CGGCATCAAC GGCGAGACCAC TCAATGCAAT TCATTTGGAT CC	1250 1310 1370 1430 1442

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 328 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Lys Trp Leu Glu Glu Ser Ile Met Ala Lys Arg Gly Val Gly Ala 1 5 10 15
Gly Arg Lys Pro Val Thr His His Leu Thr Glu Glu Met Gln Lys Glu 20 25 30
Phe His Tyr Thr Ile Gly Pro Tyr Ser Thr Pro Val Leu Thr Ile Glu 35 40 45
Pro Gly Asp Arg Ile Ile Val Asp Thr Arg Asp Ala Phe Glu Gly Ala 50 55 60
Ile Asn Ser Glu Gln Asp Ile Pro Ser Gln Leu Leu Lys Met Pro Phe 65 70 75 80
Leu Asn Pro Gln Asn Gly Pro Ile Met Val Asn Gly Ala Glu Lys Gly 85 90 95
Asp Val Leu Ala Val Tyr Ile Glu Ser Met Leu Pro Arg Gly Val Asp 100 105 110
Pro Tyr Gly Ile Cys Ala Met Ile Pro His Phe Gly Gly Leu Thr Gly 115 120 125
Thr Asp Leu Thr Ala Met Leu Asn Asp Pro Leu Pro Glu Lys Val Arg 130 135 140

Met Ile Lys Leu Asp Ser Glu Lys Val Tyr Trp Ser Lys Arg His Thr
 145 150 155 160

Leu Pro Tyr Lys Pro His Ile Gly Thr Leu Ser Val Ser Pro Glu Ile
 165 170 175

Asp Ser Ile Asn Ser Leu Thr Pro Asp Asn His Gly Gly Asn Met Asp
 180 185 190

Val Pro Asp Ile Gly Pro Gly Ser Ile Thr Tyr Leu Pro Val Arg Ala
 195 200 205

Pro Gly Gly Arg Leu Phe Ile Gly Asp Ala His Ala Cys Gln Gly Asp
 210 215 220

Gly Glu Ile Cys Gly Thr Ala Val Glu Phe Ala Ser Ile Thr Thr Ile
 225 230 235 240

Lys Val Asp Leu Ile Lys Asn Trp Gln Leu Ser Trp Pro Arg Met Glu
 245 250 255

Asn Ala Glu Asn Ile Met Ser Ile Gly Ser Ala Arg Pro Leu Glu Asp
 260 265 270

Ala Thr Arg Ile Ala Tyr Arg Asp Leu Ile Tyr Trp Leu Val Glu Asp
 275 280 285

Phe Gly Phe Glu Gln Trp Asp Ala Tyr Met Leu Leu Ser Gln Cys Gly
 290 295 300

Lys Val Arg Leu Gly Asn Met Val Asp Pro Lys Tyr Thr Val Gly Ala
 305 310 315 320

Met Leu Asn Lys Asn Leu Leu Val
 325

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not known
- (D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

- (B) STRAIN: PRS1
- (C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met Lys Trp Leu Glu Glu Ser Ile Met Ala Lys Arg Gly Val Gly Ala
 1 5 10 15

Ser Arg Lys Pro
 20

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not known
- (D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

- (B) STRAIN: PRS1
- (C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Val Tyr Trp Ser Lys
1 5

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not known
- (D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

- (B) STRAIN: PRS1
- (C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Lys Pro Val Thr His His Leu Thr Glu Glu Met Gln Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not known
- (D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

- (B) STRAIN: PRS1
- (C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Tyr Thr Val Gly Ala Met Leu Asn Lys
1 5

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not known

(D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

(B) STRAIN: PRS1

(C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met Glu Asn Ala Glu Asn Ile Met Ser Ile Gly Ser Ala Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not known

(D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

(B) STRAIN: PRS1

(C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Trp Leu Glu Glu Ser Ile Met Ala Lys
1 5

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not known

(D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

(B) STRAIN: PRS1

(C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Met Pro Phe Leu Asn Pro Gln Asn Gly Pro Ile Met Val Asn Gly Ala
1 5 10 15

Glu Lys

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS: not known
- (D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

- (B) STRAIN: PRS1
- (C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Asp Ala Phe Glu Gly Ala Ile Asn Ser Glu Gln Asp Ile Pro Ser Gln
1 5 10 15

Leu Leu Lys

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not known
- (D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

- (B) STRAIN: PRS1
- (C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Glu Phe His Tyr Thr Ile Gly Pro Tyr Ser Thr Pro Val Leu Thr Ile
1 5 10 15

Glu Pro Gly Asp Arg
20

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not known
- (D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

- (B) STRAIN: PRS1
- (C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Leu Phe Ile Gly Asp Ala His Ala Glu Gln Gly Asp Gly Glu Ile Glu

1

5

10

15

Gly Thr Ala Val Glu Phe Ala
20

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not known
 - (D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

- (vi) ORIGIN:
- (B) STRAIN: PRS1
 - (C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Gly Asp Val Leu Ala Val Tyr Ile Glu Ser Met Leu Pro Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 33 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not known
 - (D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

- (vi) ORIGIN:
- (C) INDIVIDUAL/ISOLATE: PRS1

(vii) PROVENANCE:

- (B) CLONE(S): PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Gly Val Asp Pro Tyr Gly Ile Glu Ala Met Ile Pro His Phe Gly Gly
1 5 10 15

Leu Thr Gly Thr Asp Leu Thr Ala Met Leu Asn Asp Gin Leu Gin Pro
20 25 30

Lys